

SEQUENCE LISTING

(1) GENERAL INFORMATION

- (i) APPLICANT: Hillman, Jennifer L.  
Goli, Surya K.
- (ii) TITLE OF THE INVENTION: NOVEL TUMORIGENESIS PROTEIN
- (iii) NUMBER OF SEQUENCES: 3
- (iv) CORRESPONDENCE ADDRESS:
  - (A) ADDRESSEE: Incyte Genomics, Inc.
  - (B) STREET: 3160 Porter Drive
  - (C) CITY: Palo Alto
  - (D) STATE: CA
  - (E) COUNTRY: USA
  - (F) ZIP: 94304
- (v) COMPUTER READABLE FORM:
  - (A) MEDIUM TYPE: Diskette
  - (B) COMPUTER: IBM Compatible
  - (C) OPERATING SYSTEM: DOS
  - (D) SOFTWARE: FastSEQ for Windows Version 2.0
- (vi) CURRENT APPLICATION DATA:
  - (A) APPLICATION NUMBER: To Be Assigned
  - (B) FILING DATE: Herewith
  - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
  - (A) APPLICATION NUMBER: 09/183,825
  - (B) FILING DATE: October 30, 1998
- (vii) PRIOR APPLICATION DATA:
  - (A) APPLICATION NUMBER: 08/822,260
  - (B) FILING DATE: March 20, 1997
- (viii) ATTORNEY/AGENT INFORMATION:
  - (A) NAME: Billings, Lucy J.
  - (B) REGISTRATION NUMBER: 36,749
  - (C) REFERENCE/DOCKET NUMBER: PF-0247-2 CON
- (ix) TELECOMMUNICATION INFORMATION:
  - (A) TELEPHONE: 650-855-0555
  - (B) TELEFAX: 650-845-4166
  - (C) TELEX:

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 195 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (vii) IMMEDIATE SOURCE:
  - (A) LIBRARY: UTRSNOT02
  - (B) CLONE: 2267574

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Met Glu Leu Ser Glu Ser Val Gln Lys Gly Phe Gln Met Leu Ala Asp  
 1 5 10 15  
 Pro Arg Ser Phe Asp Ser Asn Ala Phe Thr Leu Leu Arg Ala Ala  
 20 25 30  
 Phe Gln Ser Leu Leu Asp Ala Gln Ala Asp Glu Ala Val Leu Asp His  
 35 40 45  
 Pro Asp Leu Lys His Ile Asp Pro Val Val Leu Lys His Cys His Ala  
 50 55 60  
 Ala Ala Ala Thr Tyr Ile Leu Glu Ala Gly Lys His Arg Ala Asp Lys  
 65 70 75 80  
 Ser Thr Leu Ser Thr Tyr Leu Glu Asp Cys Lys Phe Asp Arg Glu Arg  
 85 90 95  
 Ile Glu Leu Phe Cys Thr Glu Tyr Gln Asn Asn Lys Asn Ser Leu Glu  
 100 105 110  
 Ile Leu Leu Gly Ser Ile Gly Arg Ser Leu Pro His Ile Thr Asp Val  
 115 120 125  
 Ser Trp Arg Leu Glu Tyr Gln Ile Lys Thr Asn Gln Leu His Arg Met  
 130 135 140  
 Tyr Arg Pro Ala Tyr Leu Val Thr Leu Ser Val Gln Asn Thr Asp Ser  
 145 150 155 160  
 Pro Ser Tyr Pro Glu Ile Ser Phe Ser Cys Ser Met Glu Gln Leu Gln  
 165 170 175  
 Asp Leu Val Gly Lys Leu Lys Asp Ala Ser Lys Ser Leu Glu Arg Ala  
 180 185 190  
 Thr Gln Leu  
 195

## (2) INFORMATION FOR SEQ ID NO:2:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 751 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (vii) IMMEDIATE SOURCE:

- (A) LIBRARY: UTRSNOT02
- (B) CLONE: 2267574

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

CGAAGTCACG GCGCGCTCAC AATGGAGCTC TCGGAGTCTG TGCAGAAAGG CTTCCAGATG 60  
 CTGGCGGATC CCCGCTCCTT CGACTCCAAC GCCTTCACGC TTCTCCTCCG GGCGGCATTC 120  
 CAGAGTCTGC TGGACGCCCA GCGGACGAG GCCGTGTTAG ATCATCCAGA CTTGAAACAT 180  
 ATCGACCCAG TGGTTTAAA ACATTGTCAT GCAGCAGCTG CAACTTACAT ACTAGAGGCA 240  
 GGAAAGCACC GAGCTGACAA GTCAACTCTA AGCACTTATC TAGAAGACTG TAAATTTGAC 300  
 AGAGAGCGAA TAGAACTGTT TTGCACGGAA TATCAGAATA ATAAGAATTC CCTAGAAATC 360  
 CTACTGGGAA GTATAGGCAG ATCTCTCCCT CATATAACGG ATGTTTCTTG GCGCTTGGA 420  
 TATCAGATAA AGACCAATCA ACTTCATAGG ATGTACAGAC CTGCATATTT GGTGACCTTA 480  
 AGTGACAGA ACACTGATTC CCCATCCTAT CCAGAGATTA GTTTTAGTTG CAGCATGGAA 540  
 CAATTACAGG ACTTGTTGGG GAAACTTAAA GATGCTTCGA AAAGCCTGGA AAGAGCAACT 600  
 CAGTTGTAAC TTGGGGAAGT TAACGATCCG CCCGAGTGCA GAGGAAAACC AGAAACGCCT 660  
 TGCCTTCAGC TGAACACCG TTTGTGCGAG CTGGATGTCC TTTTCAGTAG AAAAGAATTT 720  
 TCCTTTTGAA TTTATACCAT TCANCAATTT T 751

## (2) INFORMATION FOR SEQ ID NO:3:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 195 amino acids

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(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:  
(A) LIBRARY: GenBank  
(B) CLONE: 265569

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Met	Glu	Leu	Ser	Glu	Ser	Val	Gln	Arg	Gly	Ile	Gln	Thr	Leu	Ala	Asp	
1				5					10					15		
Pro	Gly	Ser	Phe	Asp	Ser	Asn	Ala	Phe	Ala	Leu	Leu	Leu	Arg	Ala	Ala	
			20					25					30			
Phe	Gln	Ser	Leu	Leu	Asp	Ala	Arg	Ala	Asp	Glu	Ala	Ala	Leu	Asp	His	
		35					40					45				
Pro	Tyr	Leu	Lys	Gln	Ile	Asp	Pro	Val	Val	Leu	Lys	His	Cys	His	Ala	
	50					55					60					
Ala	Ala	Ala	Thr	Cys	Ile	Leu	Glu	Ala	Gly	Lys	His	Gln	Val	Asp	Lys	
65					70					75				80		
Ser	Thr	Leu	Ser	Thr	Tyr	Leu	Glu	Asp	Cys	Lys	Phe	Asp	Arg	Glu	Arg	
			85						90					95		
Ile	Glu	Leu	Phe	Cys	Thr	Glu	Tyr	Gln	Asn	Asn	Lys	Asn	Ser	Leu	Glu	
			100					105						110		
Thr	Leu	Leu	Gly	Ser	Ile	Gly	Arg	Ser	Leu	Pro	His	Ile	Thr	Asp	Val	
		115					120						125			
Ser	Trp	Arg	Leu	Glu	Tyr	Gln	Ile	Lys	Thr	Asn	Gln	Leu	His	Lys	Met	
	130					135					140					
Tyr	Arg	Pro	Gly	Tyr	Leu	Val	Thr	Leu	Asn	Val	Glu	Asn	Asn	Asp	Ser	
145				150						155				160		
Gln	Ser	Tyr	Pro	Glu	Ile	Asn	Phe	Ser	Cys	Asn	Met	Glu	Gln	Leu	Gln	
			165						170					175		
Asp	Leu	Val	Gly	Lys	Leu	Lys	Asp	Ala	Ser	Lys	Ser	Leu	Glu	Arg	Ala	
		180						185						190		
Thr	Gln	Leu														
		195														